

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/601,311A

Source: 1FW16

Date Processed by STIC: 7/19/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 07/19/2006

PATENT APPLICATION: US/10/601,311A

TIME: 09:07:20

Input Set : F:\AKT3-5001-C1 Substitute Seq Listing.ST25.txt

Output Set: N:\CRF4\07192006\J601311A.raw

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3 <110> APPLICANT: Takeda San Diego, Inc.
5 <120> TITLE OF INVENTION: CRYSTALLIZATION OF AKT3
7 <130> FILE REFERENCE: AKT3-5001-C1
9 <140> CURRENT APPLICATION NUMBER: 10/601,311A
10 <141> CURRENT FILING DATE: 2003-06-20
12 <150> PRIOR APPLICATION NUMBER: 60/400,207
13 <151> PRIOR FILING DATE: 2002-07-31
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 479
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: MISC_FEATURE
27 <222> LOCATION: (1)..(479)
28 <223> OTHER INFORMATION: Amino acid sequence for full length human wild type AKT3
30 <300> PUBLICATION INFORMATION:
31 <308> DATABASE ACCESSION NO: Genbank/NP_005456
32 <309> DATABASE ENTRY DATE: 2002-04-04
33 <313> RELEVANT RESIDUES: (1)..(461)
35 <400> SEQUENCE: 1
37 Met Ser Asp Val Thr Ile Val Lys Glu Gly Trp Val Gln Lys Arg Gly
38 1 5 10 15
41 Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp
42 20 25 30
45 Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
46 35 40 45
49 Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
50 50 55 60
53 Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
54 65 70 75 80
57 Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
58 85 90 95
61 Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
62 100 105 110
65 Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
66 115 120 125
69 Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr
70 130 135 140
73 Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly
74 145 150 155 160
77 Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met

```

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78          165          170          175
81 Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His
82          180          185          190
85 Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu
86          195          200          205
89 Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val
90          210          215          220
93 Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu
94 225          230          235          240
97 Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val
98          245          250          255
101 Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu
102          260          265          270
105 Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr
106          275          280          285
109 Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys
110          290          295          300
113 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp
114 305          310          315          320
117 Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met
118          325          330          335
121 Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu
122          340          345          350
125 Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr
126          355          360          365
129 Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp
130          370          375          380
133 Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met
134 385          390          395          400
137 Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys
138          405          410          415
141 Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr
142          420          425          430
145 Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro
146          435          440          445
149 Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg
150          450          455          460
153 Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu
154 465          470          475
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 978
159 <212> TYPE: DNA
160 <213> ORGANISM: Homo sapiens
163 <220> FEATURE:
164 <221> NAME/KEY: misc_feature
165 <222> LOCATION: (1)..(978)
166 <223> OTHER INFORMATION: Human cDNA sequence encoding residues 136-461 of AKT3
168 <400> SEQUENCE: 2
169 tctacaacc atcataaaag aaagacaatg aatgattttg actatttgaa actactaggt      60

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Output Set: N:\CRF4\07192006\J601311A.raw

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171 aaaggcactt ttgggaaagt ttttttggtt cgagagaagg caagtggaaa atactatgct 120
173 atgaagattc tgaagaaaga agtcattatt gcaaaggatg aagtggcaca cactctaact 180
175 gaaagcagag tattaaagaa cactagacat ccctttttta catccttgaa atattccttc 240
177 cagacaaaag accgtttgtg ttttgtgatg gaatatgtta atggggggcga gctgtttttc 300
179 cttttgtcga gagagcgggt gttctctgag gaccgcacac gtttctatgg tgcagaaatt 360
181 gtctctgcct tggactatct acattccgga aagatttgtt accgtgatct caagttggag 420
183 aatctaatac tggacaaaga tggccacata aaaattacag attttggact ttgcaaagaa 480
185 gggatcacag atgcagccac catgaagaca ttctgtggca ctccagaata tctggcacca 540
187 gaggtgttag aagataatga ctatggccga gcagtagact ggtggggcct aggggttgtc 600
189 atgtatgaaa tgatgtgtgg gaggttacct ttctacaacc aggaccatga gaaacttttt 660
191 gaattaatat taatggaaga cattaatttt cctcgaacac tctcttcaga tgcaaaatca 720
193 ttgctttcag ggctcttgat aaaggatcca aataaacgcc ttggtggagg accagatgat 780
195 gcaaaagaaa ttatgagaca cagtttcttc tctggagtaa actggcaaga tgtatatgat 840
197 aaaaagcttg tacctccttt taaacctcaa gtaacatctg agacagatac tagatatttt 900
199 gatgaagaat ttacagctca gactattaca ataacaccac ctgaaaaata tgatgaggat 960
201 ggtatggact gcatggac

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204 &lt;210&gt; SEQ ID NO: 3

205 &lt;211&gt; LENGTH: 556

206 &lt;212&gt; TYPE: PRT

207 &lt;213&gt; ORGANISM: Artificial

209 &lt;220&gt; FEATURE:

210 <223> OTHER INFORMATION: Amino acid sequence for residues 136-461 of AKT3 with a cleavable

211 intein tag and cleavage site

214 &lt;220&gt; FEATURE:

215 &lt;221&gt; NAME/KEY: MISC\_FEATURE

216 &lt;222&gt; LOCATION: (1)..(226)

217 &lt;223&gt; OTHER INFORMATION: Cleavable N-terminal intein tag

219 &lt;220&gt; FEATURE:

220 &lt;221&gt; NAME/KEY: MISC\_FEATURE

221 &lt;222&gt; LOCATION: (227)..(230)

222 &lt;223&gt; OTHER INFORMATION: CRSL cleavage site

224 &lt;220&gt; FEATURE:

225 &lt;221&gt; NAME/KEY: MISC\_FEATURE

226 &lt;222&gt; LOCATION: (231)..(556)

227 &lt;223&gt; OTHER INFORMATION: Amino acid sequence for resisues 136-461 of AKT3

229 &lt;400&gt; SEQUENCE: 3

231 Met Lys Ile Glu Glu Gly Lys Leu Thr Asn Pro Gly Val Ser Ala Trp

232 1 5 10 15

235 Gln Val Asn Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly

236 20 25 30

239 Lys Thr Tyr Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu

240 35 40 45

243 Pro Ser Asn Val Pro Ala Leu Trp Gln Leu Gln Asn Asn Gly Asn Asn

244 50 55 60

247 Gly Leu Glu Leu Arg Glu Ser Gly Ala Ile Ser Gly Asp Ser Leu Ile

248 65 70 75 80

251 Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp

252 85 90 95

255 Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu

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Output Set: N:\CRF4\07192006\J601311A.raw

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256          100          105          110
259 Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val
260          115          120          125
263 Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn
264          130          135          140
267 His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser
268 145          150          155          160
271 Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu
272          165          170          175
275 Gln Leu Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile Tyr Trp
276          180          185          190
279 Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val Phe Asp
280          195          200          205
283 Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile Ile Val
284          210          215          220
287 His Asn Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met
288 225          230          235          240
291 Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys
292          245          250          255
295 Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys
296          260          265          270
299 Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr
300          275          280          285
303 Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr
304          290          295          300
307 Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met
308 305          310          315          320
311 Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg
312          325          330          335
315 Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser
316          340          345          350
319 Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys
320          355          360          365
323 Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp
324          370          375          380
327 Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr
328 385          390          395          400
331 Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn
332          405          410          415
335 Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr
336          420          425          430
339 Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys
340          435          440          445
343 Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu
344          450          455          460
347 Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro
348 465          470          475          480
351 Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg
352          485          490          495

```

## RAW SEQUENCE LISTING

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Input Set : F:\AKT3-5001-C1 Substitute Seq Listing.ST25.txt

Output Set: N:\CRF4\07192006\J601311A.raw

355 His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys  
 356 500 505 510  
 359 Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg  
 360 515 520 525  
 363 Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro  
 364 530 535 540  
 367 Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp  
 368 545 550 555  
 371 <210> SEQ ID NO: 4  
 372 <211> LENGTH: 330  
 373 <212> TYPE: PRT  
 374 <213> ORGANISM: Artificial  
 376 <220> FEATURE:  
 377 <223> OTHER INFORMATION: CRSL fused to the N-terminal of amino acid residues 136-461  
 of  
 378 AKT3  
 381 <220> FEATURE:  
 382 <221> NAME/KEY: MISC\_FEATURE  
 383 <222> LOCATION: (1)..(4)  
 384 <223> OTHER INFORMATION: CRSL cleavage site  
 386 <220> FEATURE:  
 387 <221> NAME/KEY: MISC\_FEATURE  
 388 <222> LOCATION: (5)..(330)  
 389 <223> OTHER INFORMATION: Amino acid sequence for residues 136-461 of AKT3  
 391 <400> SEQUENCE: 4  
 393 Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met Asn Asp  
 394 1 5 10 15  
 397 Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile  
 398 20 25 30  
 401 Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys Ile Leu  
 402 35 40 45  
 405 Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr Leu Thr  
 406 50 55 60  
 409 Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr Ser Leu  
 410 65 70 75 80  
 413 Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met Glu Tyr  
 414 85 90 95  
 417 Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe  
 418 100 105 110  
 421 Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu  
 422 115 120 125  
 425 Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys Leu Glu  
 426 130 135 140  
 429 Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly  
 430 145 150 155 160  
 433 Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr Phe Cys  
 434 165 170 175  
 437 Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr  
 438 180 185 190  
 441 Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/19/2006  
PATENT APPLICATION:    US/10/601,311A      TIME: 09:07:21

Input Set : F:\AKT3-5001-C1 Substitute Seq Listing.ST25.txt  
Output Set: N:\CRF4\07192006\J601311A.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4

VERIFICATION SUMMARY

DATE: 07/19/2006

PATENT APPLICATION: US/10/601,311A

TIME: 09:07:21

Input Set : F:\AKT3-5001-C1 Substitute Seq Listing.ST25.txt

Output Set: N:\CRF4\07192006\J601311A.raw